

Fig 1

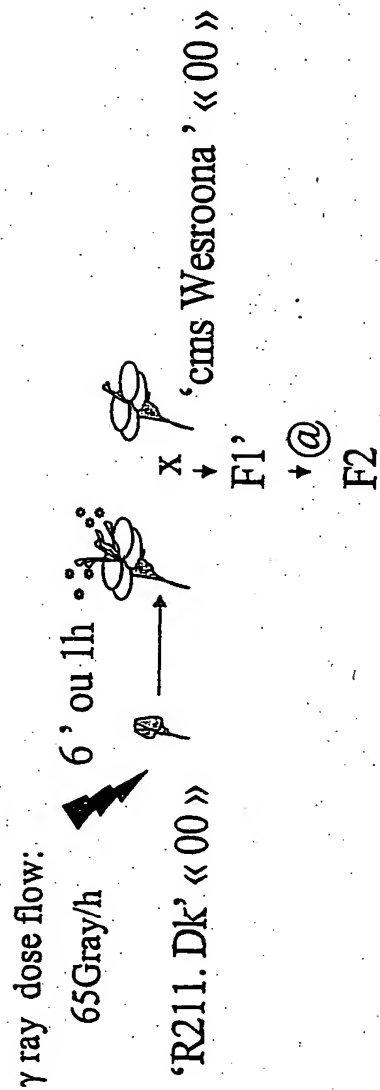


Fig 2

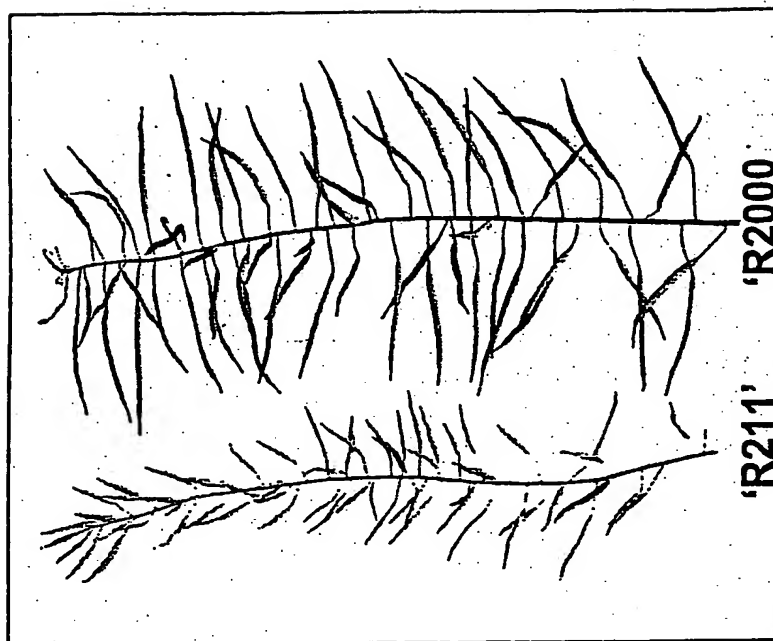


Fig. 1: Seed set on 'R211' and 'R2000'

Fig 3

Genotype	Selfings	Test Crosses
Drakkar	29.3	
Pactol	23.1	
R211	11.2	25.5
R2000	26.5 (24.0 – 31.1)	27.0 (24.0 – 28.7)

Fig 4

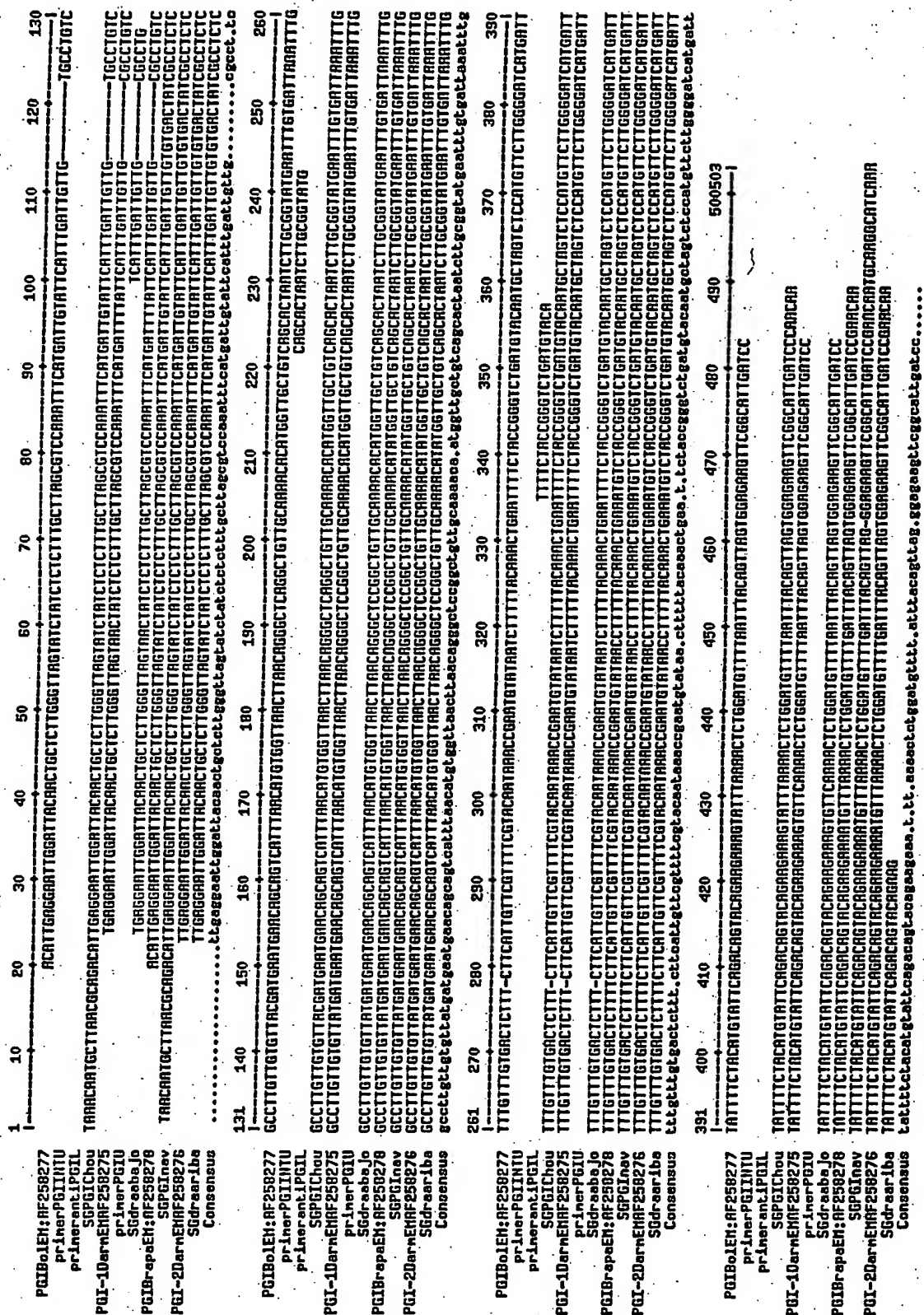
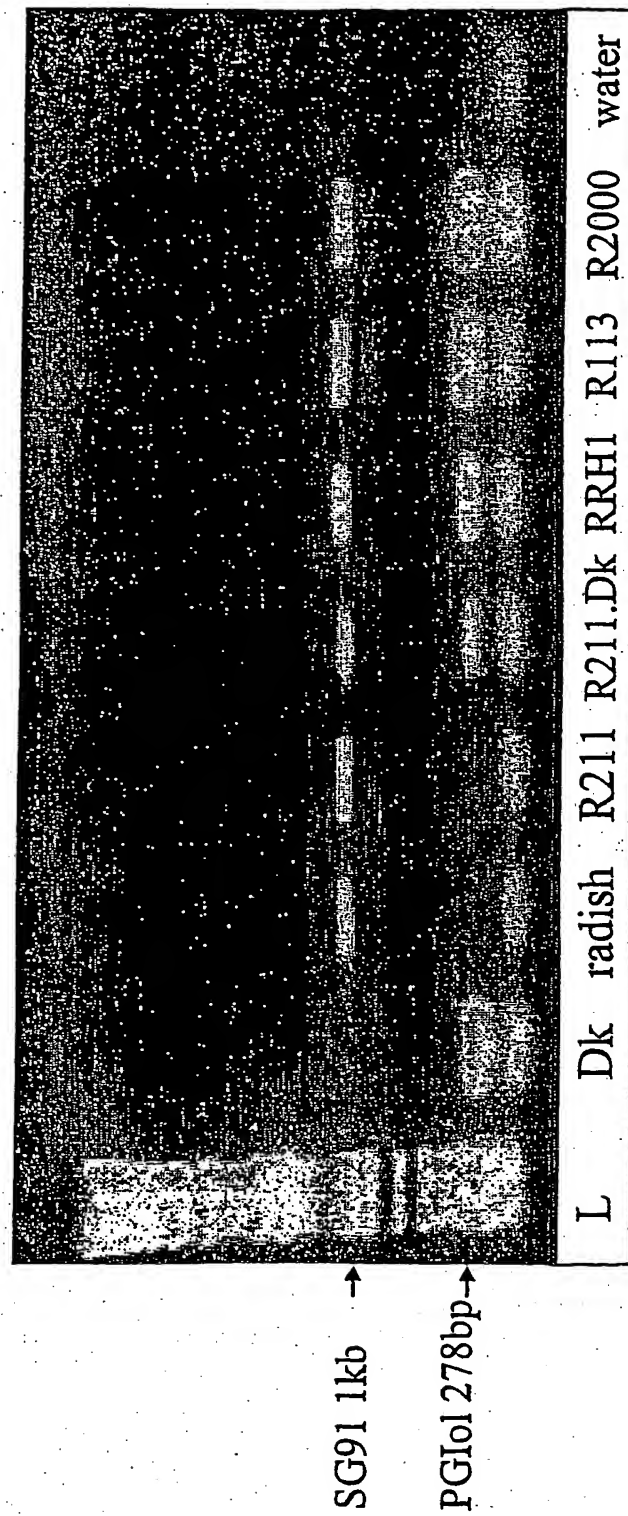


Fig 5



[illegible]

**MseI sites**



## T in Drakkar and R2000

**MseI restriction enzyme cut DNA sequences at the T/TAA sites (\*)**

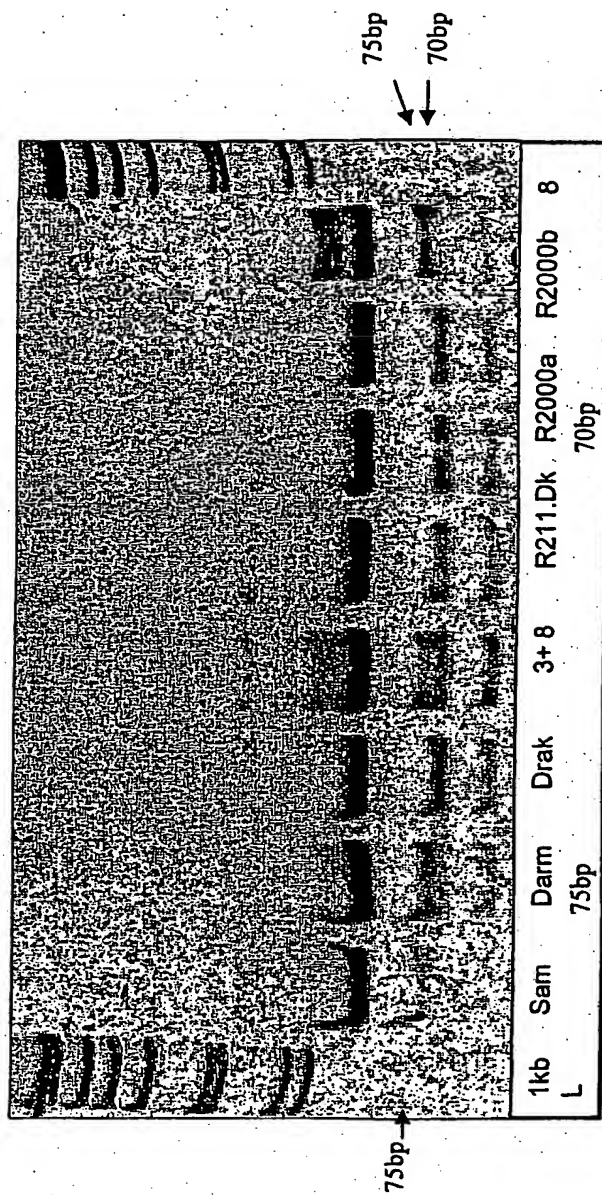


Fig 7

Fig 8

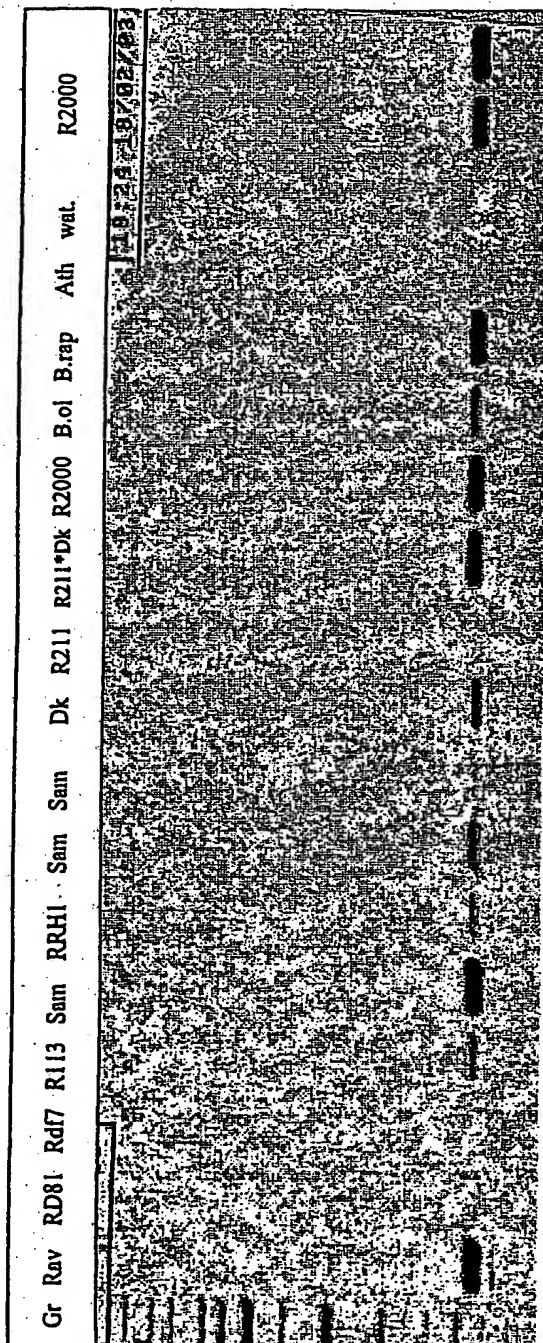




Fig 9

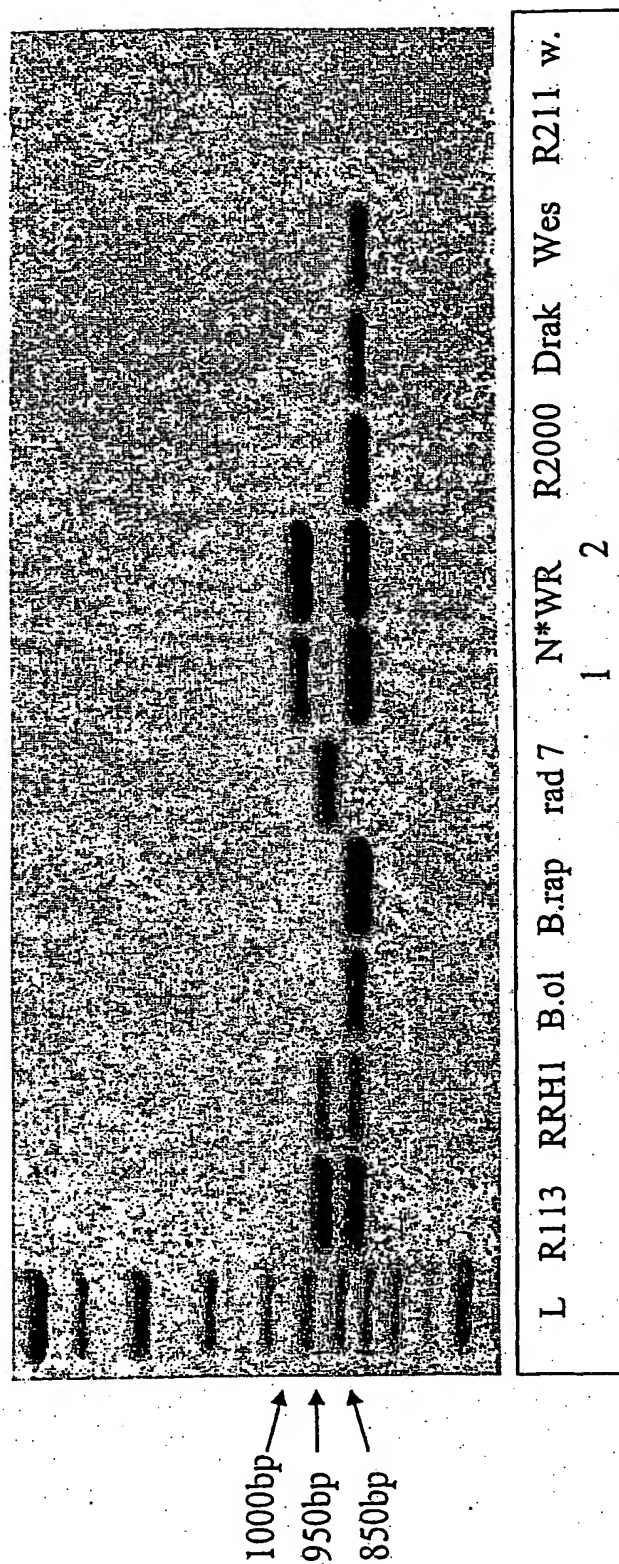


Fig 10

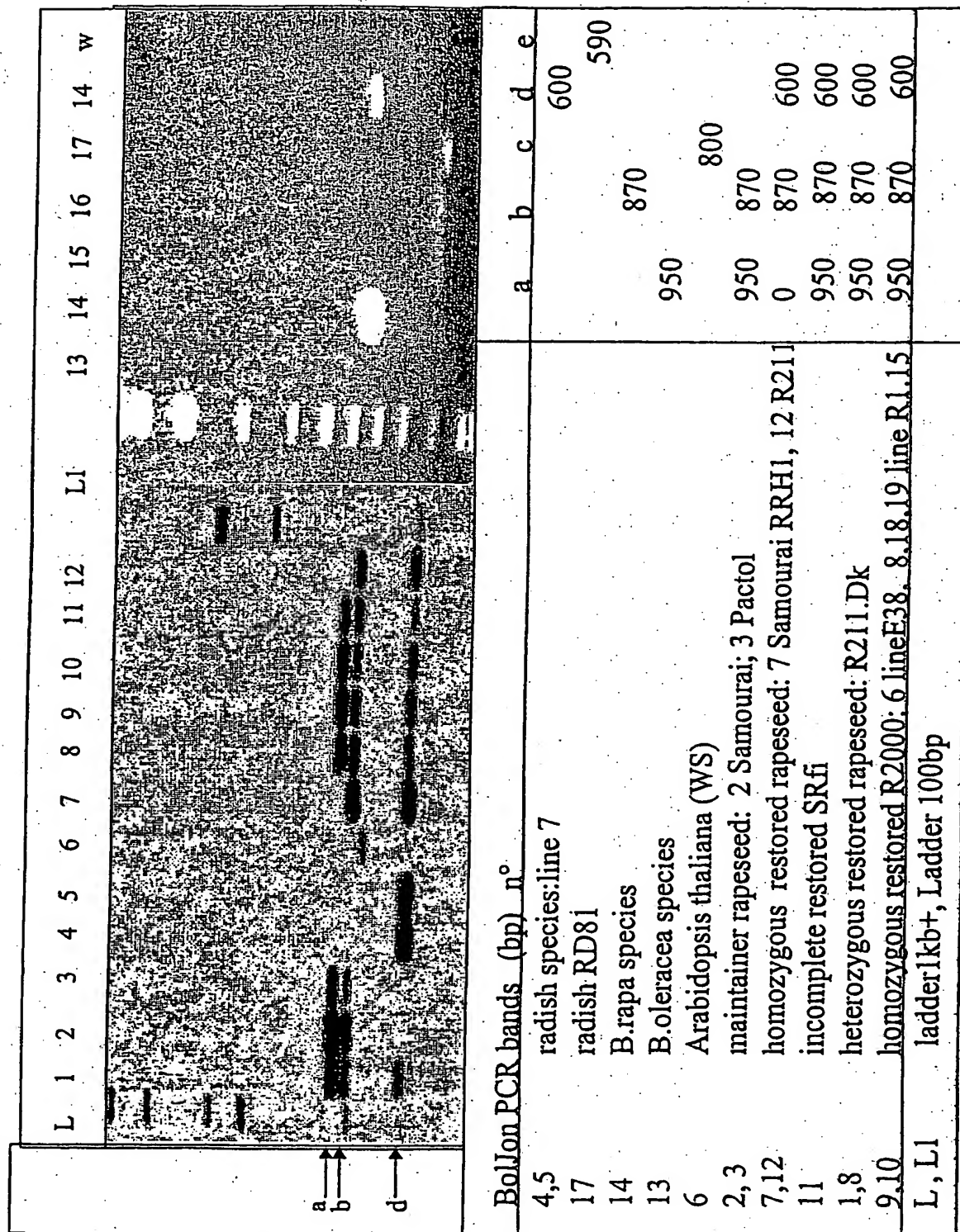
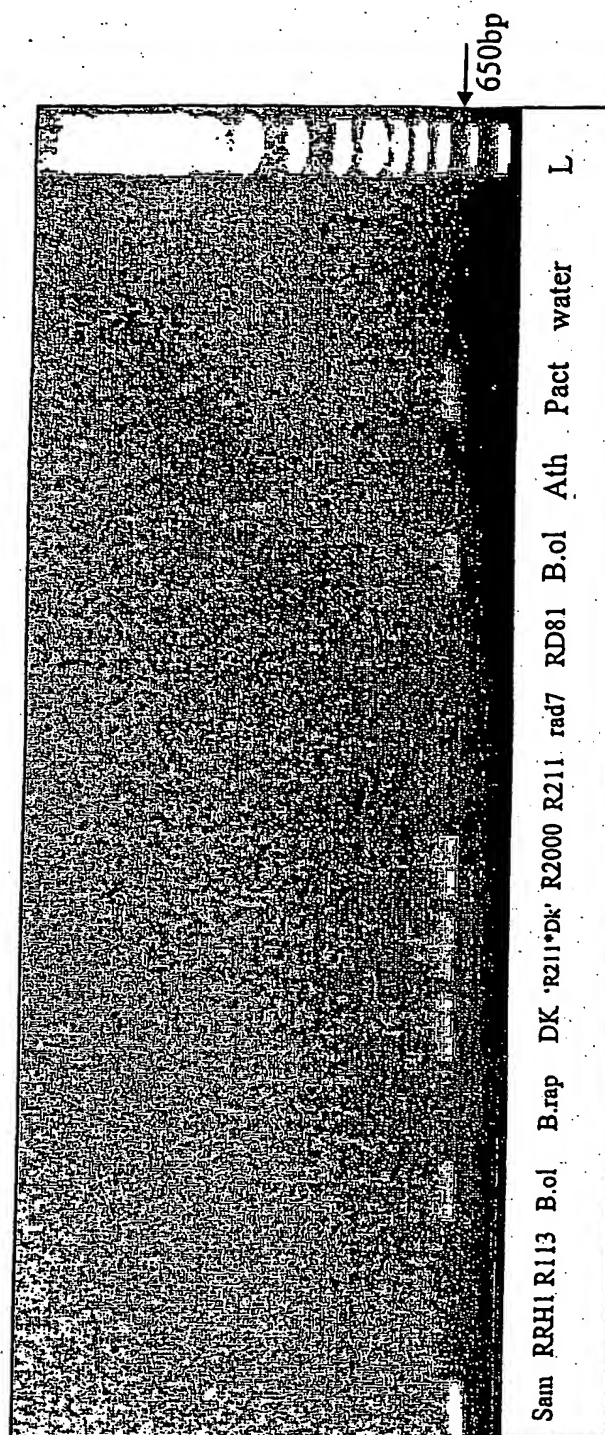


Fig 11



The CP418 band (about 650bp) specific to the *B. oleracea* genome.

It is present in B.ol, B.napus (Samourai, Drakkar, Pactol and the heterozygous R211\*Dk)

It is absent from the restored rapeseed (RRH, R113 and R211)

It is present in the homozygous R2000.



Figure 13 (a)

	51		81 PGIol U --> 100
consePGIintUNTDrakka	.....	.....	.....
consensWesrPGI	.....	.....	.....
consePGIintUNTR113	.....	.....	.....
consePGIintUNTRBrapaA	.....	.....	.....
ConsePGIintUNTRRH1	.....	.....	.....
PGIBo-EM:AF258277	TTGCTTAGCG	TCCAAATTTTC	ATGATTGTAT TCATTGATT GTTGTG...
PGIBra-EM:AF258278	TTGCTTAGCG	TCCAAATTTTC	ATGATTGTAT TCATTGATT GTTGTGTGAC
consePGIintUNTBolera	.....	.....	.....
consePGIintUNTR2000	.....	TTG...	TCATT.GA...TTGT.TGCG
Consensus			1
	101	----	150
consePGIintUNTDrakka	.....	.....GTCG	TTTGTGTTGGTG AGT.GAACAG CAGTCATTTA
consensWesrPGI	.....	GCCTGTTTG	TGTTATGATG AAT.GAACAG CAGTCATTTA
consePGIintUNTR113	.....	GCCCGGTTG	.....G TAT.GAAACG CAG.CATTTA
consePGIintUNTRBrapaA	.....	.....	.....G CAGTCATTTA
ConsePGIintUNTRRH1	.....	.....	.....CG TGTGAGAAG CAG.CATTTA
PGIBo-EM:AF258277	.....	CCTG	TGCGCTTGTG TGTTA.GATG AAT.GAACAG CAGTCATTTA
PGIBra-EM:AF258278	TATCGCCTC.	TGCGCTTGTG	TGTTATGATG AAT.GAACAG CAGTCATTTA
consePGIintUNTBolera	.....	.....	.....
consePGIintUNTR2000	.....	CCTG	TGCGCTTGTG TGTTATGATG AAT.GAACA. CAGTCATTTA
Consensus	.....	....	.....t.g .....g....t.gaa.ag cagtcattta
	151		200
		MseI restriction site	
consePGIintUNTDrakka	ACATG.TGGT	TAACCTAACA	GGGCTCCGGC TGTGCAAAA CACATGGTTG
consensWesrPGI	ACATG.TGGT	TAACCTAACA	GGGCTCCGGC TGTGCAAAA CACATGGTTG
consePGIintUNTR113	ACATG.TGGT	.AACTGAACA	GGGCTCCGGC TGTGCCC.. CTAAGGGTTG
consePGIintUNTRBrapaA	ACATGGTGGT	TAACCTGAACA	GGGCTCCGGC TGTGCAAAA CACATGGTTG
ConsePGIintUNTRRH1	ACATG..GGT	.ACTGAACA	GGGC.CCGGC TGTGCAA.. .ACAG...TG
PGIBo-EM:AF258277	ACATG.TGGT	TAACCTAACA	GGGCTCAGGC TGTGCAAAA CACATGGTTG
PGIBra-EM:AF258278	ACATG.TGGT	TAACCTAACA	GGGCTCCGGC TGTGCAAAA CATATGGTTG
consePGIintUNTBolera	.....	.....	.....C TGTGCAAAA CACATGGTTG
consePGIintUNTR2000	ACATG.TGGT	TAACCTAACA	GGGCTCCGGC TGTGCAAAA CACATGGTTG
Consensus	acatg.tggt	taact.aaca	gggctccggc tggtgcaaaa cacatggttg
	2		
	201	PGI int U ---->	250
consePGIintUNTDrakka	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
consensWesrPGI	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
consePGIintUNTR113	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
consePGIintUNTRBrapaA	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
ConsePGIintUNTRRH1	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
PGIBo-EM:AF258277	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
PGIBra-EM:AF258278	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
consePGIintUNTBolera	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
consePGIintUNTR2000	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT
Consensus	ctgtcagcac	taatcttgc ggtatg	aatt tgtgattaaa tttgtttgt
	251		300
consePGIintUNTDrakka	TGTGACTCTT	T.CTTTCATTG	TTCGTTTTTCG TACAATAAAC CGAATGTATA
consensWesrPGI	TGTGACTCTT	T.CTTTCATTG	TTCGTTTTTCG TACAATAAAC CGAATGTATA
consePGIintUNTR113	TGCGACTCTT	T.CTTTCATTG	TTCGTTTTTCG TACAATAAAC ..AATGTATA
consePGIintUNTRBrapaA	TGCGACTCTT	T.CTTTCATTG	TTCGTTTTTCG TACAATAAAC ..AATGTATA
ConsePGIintUNTRRH1	TGCGACTCTT	T.CTTTCATTG	TTCGTTTTTCG TACAATAAAC ..AATGTATA
PGIBo-EM:AF258277	TGTGACTCTT	T.CTTTCATTG	TTCGTTTTTCG TACAATAAAC CGAATGTATA
PGIBra-EM:AF258278	TGTGACTCTT	TTCTTCATTG	TTCGTTTTTCG TACAATAAAC CGAATGTATA
consePGIintUNTBolera	TG.GACTCTT	T.CTTTCATTG	TTCGTTTTTCG TACAATAAAC CGAATGTATA
consePGIintUNTR2000	TGTGACTCTT	T.CTTTCATTG	TTCGTTTTTCG TACAATAAAC CGAATGTATA
Consensus	tg.gactctt	t.cttcattg	ttcgttttcg tacaataaac cgaatgtata
			03

Figure 13 (b)

	301	<---	PGIol antL 341	350
consePGIintUNTDrakka	ATCTTTTAC AAAC TGAA		TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consensWesrPGI	ATCTTTTAC AAAC TGAA		TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTR113	ATCTTTTAC AAAC TGAA		TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTBrapaA	ATCTTTTAC AAAC TGAA		TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
ConsePGIintUNTRRH1	ATCTTTTAC AAAC TGAA		TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
PGIBo-EM:AF258277	ATCTTTTAC AAAC TGAA		TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
PGIBra-EM:AF258278	ACCTTTTAC AAAC TGAA		AT GTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTBolera	ATCTTTTAC AAAC TGAA		TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTR2000	ATCTTTT.AC AAAC TGAA		TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
Consensus	atctttttac aaactgaa		tt ttctaccggg tctgatgtac a	atgctAGTC

201	PGI int U -->		250
consePGIintUNTDrakka	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
consensWesrPGI	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
consePGIintUNTR113	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
consePGIintUNTBrapaA	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
ConsePGIintUNTRRH1	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
PGIBo-EM:AF258277	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
PGIBra-EM:AF258278	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
consePGIintUNTBolera	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
consePGIintUNTR2000	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
Consensus	ctgtcagcac	taatcttgc ggtatg	aatt tgtgattaaa tttgtttggt

	251				300
consePGIintUNTDrakka	TGTGACTCTT	T.CTTTCATTG	TTCGTTTTTCG	TACAATAAAC	CGAATGTATA
consensWesrPGI	TGTGACTCTT	T.CTTTCATTG	TTCGTTTTTCG	TACAATAAAC	CGAATGTATA
consePGIintUNTR113	TGCGACTCTT	T.CTTTCATTG	TTCGTTTTTCG	TACAATAAAC	..AATGTATA
consePGIintUNTBrapa	TGCGACTCTT	T.CTTTCATTG	TTCGTTTTTCG	TACAATAAAC	..AATGTATA
ConsePGIintUNTRRH1	TGCGACTCTT	T.CTTTCATTG	TTCGTTTTTCG	TACAATAAAC	..AATGTATA
PGIBo-EM:AF258277	TGTGACTCTT	T.CTTTCATTG	TTCGTTTTTCG	TACAATAAAC	CGAATGTATA
PGIBra-EM:AF258278	TGTGACTCTT	TTCTTCATTG	TTCGTTTTTCG	TACAATAAAC	CGAATGTATA
consePGIintUNTBolera	TG.GACTCTT	T.CTTTCATTG	TTCGTTTTTCG	TACAATAAAC	CGAATGTATA
consePGIintUNTR2000	TGTGACTCTT	T.CTTTCATTG	TTCGTTTTTCG	TACAATAAAC	CGAATGTATA
Consensus	tg.gactctt	t.cttcattg	ttcgttttcg	tacaataaac	cgaaatgata

	301		PGIol antL 341	350
consePGIintUNTDrakka	ATCTTTTAC	AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consensWesrPGI	ATCTTTTAC	AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTR113	ATCTTTTAC	AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTBrapaA	ATCTTTTAC	AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
ConsePGIintUNTRRH1	ATCTTTTAC	AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
PGIBo-EM:AF258277	ATCTTTTAC	AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
PGIBra-EM:AF258278	ACCTTTTAC	AAACTGAA	AT GTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTBolera	ATCTTTTAC	AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTR2000	ATCTTTT.AC	AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
Consensus	atcttttttac	aaactgaa	tt tttctaccggg tctgatgtac a atctctAGTC	

	351				400
consePGIintUNTDrakka	TCCATGTTCT	TGGGGATCAT	GATTTATTTT	CTACATGTAT	TCAGACAGTA
consensWesrPGI	TCCATGTTCT	TGGGGATCAT	GATTTATTTT	CT.CATGTAT	TCAGACAGTA
consePGIintUNTR113	TCCATGTTCT	TGGGGATCAT	GATTTATTTT	CTACATGTGT	TCAGCCAGTA
consePGIintUNTBrapaA	TCCATGTTCT	TGGGGATCAT	GATTTATTTT	CTACATGTGT	TCAGCCAGTA
ConsePGIintUNTRRH1	TCCATGTTCT	TGGGGATCAT	GATTTATTTT	CTACATGTGT	TCAGCCAGTA
PGIBo-EM:AF258277	TCCATGTTCT	TGGGGATCAT	GATTTATTTT	CTACATGTAT	TCAGACAGTA
PGIBra-EM:AF258278	TCCATGTTCT	TGGGGATCAT	GATTTATTTT	CTACATGTAT	TCAGACAGTA
consePGIintUNTBolera	TCCATGTTCT	TGGGGATCAT	GATTTATTTT	CTACATGTAT	TCAGACAGTA
consePGIintUNTR2000	TCCATGTTCT	TGGGGATCAT	GATTTATTTT	CTACATGTAT	TCAGACAGTA
Consensus	TCCATGTTCT	TGGGGATCAT	GATTTATTTT	CTaCATGTAT	TCAGACAGTA

	401		450
consePGIintUNTDrakka	CAGAAGAAAG	TGTTCAAAC	TCTGGATGTT TTAATTTACA GTTAGTGGAG
consensWesrPGI	CAGAAGAAAG	TGTTCAAAC	TCTGGATGTT TTAATTTACA GTTAGTGGAG
consePGIintUNTR113	CAGAAGAAAG	TGTTTAAAC	TCTGGATGTT TTAATTTACA GTTAGTGGAG
consePGIintUNTBrapaA	CAGAAGAAAG	TGTTTAAAC	TCTGGATGTT TTAATTTACA GTTAGTGGAG
ConsePGIintUNTRRH1	CAGAAGAAAG	TGTTTAAAC	TCTGGATGTT TTAATTTACA GTTAGTGGAG
PGIBo-EM:AF258277	CAGAAGAAAG	TATTTAAAC	TCTGGATGTT TTAATTTACA GTTAGTGGAG
PGIBra-EM:AF258278	CAGAAGAAAG	TGTTTAAAC	TCTGGATGTT TTGATTTACA GTTAGTGGAG
consePGIintUNTBolera	CAGAAGAAAG	TGTTCAAAC	TCTGGATGTT TTAATTTACA GTTAGTGGAG
consePGIintUNTR2000	CAGAAGAAAG	TGTTCAAAC	TCTGGATGTT TTAATTTACA GTTAGTGGAG
Consensus	CAGAAGAAAG	TGTTCAAAC	TCTGGATGTT TTAATTTACA GTTAGTGGAG



Figure 14 (b)

	451	end of Data Base PGI sequences				500
consePGIintUNTDrakka	AAGTTCGGCA	TTGATCCGAA	CAATGCATTT	GCATTTTGGG	ACTGGGTTGG	
consensWesrPGI	AAGTTCGGCA	TTGATCCGAA	CAATGCATTT	GCATTTTGGG	ACTGGGTTGG	
consePGIintUNTR113	AAGTTCGGCA	TTGATCCGAA	CAATGCATTT	GCATTTTGGG	ACTGGGTTGG	
consePGIintUNTBrapaA	AAGTTCGGCA	TTGATCCGAA	CAATGCATTT	GCATTTTGGG	ACTGGGTTGG	
ConsePGIintUNTRRH1	AAGTTCGGCA	TTGATCCGAA	CAATGCATTT	GCATTTTGGG	ACTGGGTTGG	
PGIBo-EM:AF258277	AAGTTCGGCA	TTGATCC...	.....	.....	.....	
PGIBra-EM:AF258278	AAGTTCGGCA	TTGATCCGAA	CAA.....	.....	.....	
consePGIintUNTBolera	AAGTTCGGCA	TTGATCCGAA	CAATGCATTT	GCATTTTGGG	ACTGGGTTGG	
consePGIintUNTR2000	AAGTTCGGCA	TTGATCCGAA	CAATGCATTT	GCATTTTGGG	ACTGGGTTGG	
Consensus	AAGTTCGGCA	TTGATCCgaa	caatgcattt	gcattttggg	actggggttg	
	501					550
consePGIintUNTDrakka	TGGAAGGTAC	AGTGGTAAGT	GCTTGTTTAT	TTGGTTGTAT	TAATTTCTCG	
consensWesrPGI	TGGAAGGTAC	AGTGGTAAGT	GCTTGTTTAT	TTGGTTGTAT	TAATTTCTCG	
consePGIintUNTR113	TGGAAGGTAC	AGTGGTAAGT	GCTTGTTTAT	TTGGTTGTAT	TAATTTCTCA	
consePGIintUNTBrapaA	TGGAAGGTAC	AGTGGTAAGT	GCTTGTTTAT	TTGGTTGTAT	TAATTTCTCA	
ConsePGIintUNTRRH1	TGGAAGGTAC	AGTGGTAAGT	GCTTGTTTAT	TTGGTTGTAT	TAATTTCTCA	
PGIBo-EM:AF258277	.....	.....	.....	.....	.....	
PGIBra-EM:AF258278	.....	.....	.....	.....	.....	
consePGIintUNTBolera	TGGAAGGTAC	AGTGGTAAGT	GCTTGTTTAT	TTGGTTGTAT	TAATTTCTCG	
consePGIintUNTR2000	TGGAAGGTAC	AGTGGTAAGT	GCTTGTTTAT	TTGGTTGTAT	TAATTTCTCG	
Consensus	tggaaggtac	agtggtaagt	gcttgtttat	ttggttgtat	taatttctc	
				8	9	
	551					600
consePGIintUNTDrakka	TCCATTTCCG	CTTGCTTAGT	GTATAACTGA	AATTCTTTTG	CAGTTTGCAG	
consensWesrPGI	TCCATTTCCG	CTTGCTTAGT	GTATAACTGA	AATTCTTTTG	CAGTTTGCAG	
consePGIintUNTR113	TCCATATCCG	CTTGCTTAGT	TTATAACTGA	AATTCTTTTG	CAGTTTGCAG	
consePGIintUNTBrapaA	TCCATATCCG	CTTGCTTAGT	TTATAACTGA	AATTCTTTTG	CAGTTTGCAG	
ConsePGIintUNTRRH1	TCCATATCCG	CTTGCTTAGT	TTATAACTGA	AATTCTTTTG	CAGTTTGCAG	
PGIBo-EM:AF258277	.....	.....	.....	.....	.....	
PGIBra-EM:AF258278	.....	.....	.....	.....	.....	
consePGIintUNTBolera	TCCATTTCCG	CTTGCTTAGT	GTATAACTGA	AATTCTTTTG	CAGTTTGCAG	
consePGIintUNTR2000	TCCATTTCCG	CTTGCTTAGT	GTATAACTGA	AATTCTTTTG	CAGTTTGCAG	
Consensus	tccat.tccg	cttgcttagt	.tataactga	aattcttttg	cagtttgcag	
	10		11			
	601					650
consePGIintUNTDrakka	TGCTGTTGGA	GTCTTACCAT	TGTCTCTACA	GTATGGCTTC	TCTGTGGTTG	
consensWesrPGI	TGCTGTTGGA	GTCTTACCAT	TGTCTCTACA	GTATGGCTTC	TCTGTGGTTG	
consePGIintUNTR113	TGCTGTTGGA	GTCTTACCAT	TGTCTCTACA	GTATGGCTTC	TCCGTGGTTG	
consePGIintUNTBrapaA	TGCTGTTGGA	GTCTTACCAT	TGTCTCTACA	GTATGGCTTC	TCCGTGGTTG	
ConsePGIintUNTRRH1	TGCTGTTGGA	GTCTTACCAT	TGTCTCTACA	GTATGGCTTC	TCCGTGGTTG	
PGIBo-EM:AF258277	.....	.....	.....	.....	.....	
PGIBra-EM:AF258278	.....	.....	.....	.....	.....	
consePGIintUNTBolera	TGCTGTTGGA	GTCTTACCAT	TGTCTCTACA	GTATGGCTTC	TCTGTGGTTG	
consePGIintUNTR2000	TGCTGTTGGA	GTCTTACCAT	TGTCTCTACA	GTATGGCTTC	TCTGTGGTTG	
Consensus	tgctgttga	gtcttaccat	tgtctctaca	gtatggcttc	tc.tgtggttg	
					12	
	651					700
consePGIintUNTDrakka	AGAAGTACGG	TACCTTCTAC	TTTATAGCC	ATCTCATAAA	ATGTCTTAGG	
consensWesrPGI	AGAAGTACGG	TACCTTCTAC	TTTATAGCC	ATCTCATAAA	ATGTCTTAGG	
consePGIintUNTR113	AGAAGTACGG	TACCTTCTAC	TTTATTAGCC	ATCTCATAAA	ATGTCTTGGG	
consePGIintUNTBrapaA	AGAAGTACGG	TACCTTCTAC	TTTATTAGCC	ATCTCATAAA	ATGTCTTGGG	
ConsePGIintUNTRRH1	AGAAGTACGG	TACCTTCTAC	TTTATTAGCC	ATCTCATAAA	ATGTCTTGGG	
PGIBo-EM:AF258277	.....	.....	.....	.....	.....	
PGIBra-EM:AF258278	.....	.....	.....	.....	.....	
consePGIintUNTBolera	AGAAGTACGG	TACCTTCTAC	TTTATAGCC	ATCTCATAAA	A.GTCTTAGG	
consePGIintUNTR2000	AGAAGTACGG	TACCTTCTAC	TTTATAGCC	ATCTCATAAA	ATGTCTTAGG	
Consensus	agaagtacgg	taccttctac	tttat.agcc	atctcataaa	atgtctt.gg	
			13		14	



Figure 14 (c)

	701		750
consePGIintUNTDrakka	CATATTCTTT CTATTTTATT TTCCTCTTAA TGATTTCCTC TTTTTTTTAT		
consensWesrPGI	CATATTCTTT CTATTTTATT TTCCTCTTAA TGATTTCCTC TTTTTTTTAT		
consePGIintUNTR113	CATATTCTTT CTATTTTATT TTCCTCTGAA TGATTTCCTC TCTTTTAT..		
consePGIintUNTRapaa	CATATTCTTT CTATTTTATT TTCCTCTGAA TGATTTCCTC TCTTTTAT..		
ConsePGIintUNTRRH1	CATATTCTTT CTATTTTATT TTCCTCTGAA TGATTTCCTC TCTTTTAT..		
PGIBo-EM:AF258277	.....		
PGIBra-EM:AF258278	.....		
consePGIintUNTBolera	CATATTCTTT CTATTTTATT TTCCTCTTAA TGATTTCCTC TTTTTTTA..		
consePGIintUNTR2000	CATATTCTTT CTATTTTATT TCCCTCTTAA TGATTTCCTC TTTTTTTTAT		
Consensus	catattcttt ctattttatt ttcctctt aa tgatttcctc tttttt..	15	16 17
	751		800
consePGIintUNTDrakka	TGCATTCCCG TTTTATTTTC AAAAGTTGTT ACTGTCTCTA AATCAAGAAG		
consensWesrPGI	TGCATTCCCG TTTTATTTTC AAAAGTTGTT ACTGTCTCTA AATCAAGAAG		
consePGIintUNTR113	TGCATTCCCG TTTTATTTTC AAAAGTTGTC ACTGTCTCTA AATCAAGAAG		
consePGIintUNTRapaa	TGCATTCCCG TTTTATTTTC AAAAGTTGTC ACTGTCTCTA AATCAAGAAG		
ConsePGIintUNTRRH1	TGCATTCCCG TTTTATTTTC AAAAGTTGTC ACTGTCTCTA AATCAAGAAG		
PGIBo-EM:AF258277	.....		
PGIBra-EM:AF258278	.....		
consePGIintUNTBolera	TGCATTCCCG TTTTATTT.C AAAAGTTGTC CGGCCCCCTA AATCAAGAAG		
consePGIintUNTR2000	TGCATTCCCG TTTTATTTTC AAAAGTTGTT ACTGTCTCTA AATCAAGAAG		
Consensus	tgcatcccg ttttattttc aaaagttgt. actgtctcta aatcaagaag		
	801		850
consePGIintUNTDrakka	AAACCTTCTT AGTAGATCCA GTGATATTC AGCCTTTTCT AAATTGGACT		
consensWesrPGI	AAACCTTCTT AGTAGATCCA GTGATATTC AGCCTTTTCT AAATTGGACT		
consePGIintUNTR113	AAACCTTCTT AGTAGATCCA GTTGATATTC AGCCTTTTCT AAATTGGACT		
consePGIintUNTRapaa	AAACCTTCTT AGTAGATCCA G.TGATATTC AGCCTTTTCT AAATTGGACT		
ConsePGIintUNTRRH1	AAACCTTCTT AGTAGATCCA GTTGATATTC AGCCTTTTCT AAATTGGACT		
PGIBo-EM:AF258277	.....		
PGIBra-EM:AF258278	.....		
consePGIintUNTBolera	AAACCTTTCT AGGA...CCA GA....CTCC ACCCTTTTCT AAATTGGACT		
consePGIintUNTR2000	AAACCTTCTT AGTAGATCCA GTGATATTC AGCCTTTTCT AAATTGGACT		
Consensus	aaaccttctt agtagatcca g.tgatattc agcctttt..t aaattggact	18	19
	851		900
consePGIintUNTDrakka	GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATAGCATT TCCAGTCCCC		
consensWesrPGI	GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATAGCATT TCCAGTCCAC		
consePGIintUNTR113	GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCC..		
consePGIintUNTRapaa	GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCC..		
ConsePGIintUNTRRH1	GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCCAC		
PGIBo-EM:AF258277	.....		
PGIBra-EM:AF258278	.....		
consePGIintUNTBolera	GCAGGTTTTT AAA.GGGGGC TTCAAGCATT GATAGCATT TCCAGTCCAC		
consePGIintUNTR2000	GCAGGTTTTT AAACGGGAGC TTCAAGCATT GATAGCATT TCCAGTCCAC		
Consensus	gcagggtttt aaa.gggagc ttcaagcatt gatlagcatt tccagtcc.c	20	
	901		950
consePGIintUNTDrakka	ACC.GTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT GTGTGATTAT		
consensWesrPGI	ACC.GTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT		
consePGIintUNTR113	.CCCGTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. .GTGATTAT		
consePGIintUNTRapaa	.CCCGTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT		
ConsePGIintUNTRRH1	ACC.GTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT		
PGIBo-EM:AF258277	.....		
PGIBra-EM:AF258278	.....		
consePGIintUNTBolera	ACCCGTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT		
consePGIintUNTR2000	ACC.GTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT		
Consensus	acc.gtttga gaagaatata cccgtgagtt gcattagtt. gtgtgattat		

Figure 14 (d)

	951				1000
consePGIintUNTDrakka	ACAGTTTTTC	TTGTCTTTTT	GCTATGCCCA	TCAACACTAG	AAGATTCTGTG
consensWesrPGI	ACAGTTTT.C	TTGTCTTTTT.	GCTATGTCCA	TCAACACTAG	A.GATTCTGTG
consePGIintUNTR113	ACAGTTTT.C	TTGCCTTTTT	GCTAT..AGG	GCAAC.CTAG	A.GATTTCATG
consePGIintUNTBrapaA	ACAGTTTT.C	TTGTCTTTTT	GCTATG.TCA	TCAAC.CTAG	A.GATTTCATG
ConsePGIintUNTRRH1	ACAGTTTT.C	TTGTCTTTTT	GCTAT...AT	GCAACCCTAG	..GATTTCATG
PGIBo-EM:AF258277	.....	.....	.....	.....	.....
PGIBra-EM:AF258278	.....	.....	.....	.....	.....
consePGIintUNTBolera	ACAGTTTT.C	TTGTCTTTTT	GCTAG..TGA	TCAAC.CTAG	A.GATTCTGTG
consePGIintUNTR2000	ACAGTTTT.C	TTGTCTTTTT	GCTATGTCCA	TCAACACTAG	A.GATTCTGTG
Consensus	acagtttt.c	ttgtcttttt	gctat....a	tcaac.ctag	a.gattcttg
					21
	1001				1050
consePGIintUNTDrakka	AAGTTATTAG	TGTAGCCAAC	GCCTAGGGGG	AGGTTGGTTG	GCTGTTTTGG
consensWesrPGI	AAGTTATTAG	TGTAGTCAAC	GCA.....	.....	.....
consePGIintUNTR113	AAGTTATTAG	TGTAGTCAAC	GCAGAGGAGA	G..TTCACTG	ACGG.....
consePGIintUNTBrapaA	AAGTTATTAG	TGTAGTCAAC	GCAGAGTGAG	AGG.TGATTG	.....
ConsePGIintUNTRRH1	AAGTTATTAG	TGTAGTCAAC	GCAGAGGAGG	AGATGGTT..	.....
PGIBo-EM:AF258277	.....	.....	.....	.....	.....
PGIBra-EM:AF258278	.....	.....	.....	.....	.....
consePGIintUNTBolera	AAGTTATTAG	TGTAGTCAAC	GCATAGGAGG	AGC.....	.....
consePGIintUNTR2000	AAGTTATTAG	TGTAGTCAAC	GCATAGGGAG	AGGTGAT.GG	TGACTTTTGG
Consensus	aagttattag	tgtagtcaac	gca.agg.g.	.g.....	.....
	1051		1076		
consePGIintUNTDrakka	ACGTTTTTCAC	GTGCTCCGGG	GGGTTTTTGG	GGACCAAACC	CCCAAC
consensWesrPGI	.....	.....	.....	.....	.....
consePGIintUNTR113	.....	.....	.....	.....	.....
consePGIintUNTBrapaA	.....	.....	.....	.....	.....
ConsePGIintUNTRRH1	.....	.....	.....	.....	.....
PGIBo-EM:AF258277	.....	.....	.....	.....	.....
PGIBra-EM:AF258278	.....	.....	.....	.....	.....
consePGIintUNTBolera	.....	.....	.....	.....	.....
consePGIintUNTR2000	ACGATTTCAG	GTGCTTTAGG	GTTATTG	.....	.....

Figure 15 (a)

	51	100
EMBH44836anti	.....	.....
GCP18-5CP418L-Sams	.....	.....
GCP18-2CP418L-Wes	.....	.....
GCP18-4CP418L-R2000	.....	CP418L
conse129bal-Drak	..... AAACAAATCA AAATTCTAAA TTTCTCCA	
GCPS18-129Sam-ba2	..... AAAC TATGTA ACAAAATCA AAATTGTAAA TTTCTCCA	
GCPR18-3129R211-ba2	..... AA CCAAAATCC AAATTGTAAA TTTCTCCT	
GCP18-10129R20-ba2	..... CAAATCCA AAATTGTAAA TTTCT.CCT	
Consensus	.....	.....
	101	150
EMBH44836anti	.....	.....
GCP18-5CP418L-Sams	..... AT A.CATTTTCT GTAA	
GCP18-2CP418L-Wes	..... AGG T.AT A.CATTTTCT GTAA	
GCP18-4CP418L-R2000	..... AGG TCAT A.CATTTTCT GTAA	
conse129bal-Drak	TCACAAGGAC CTACAGAATA GAGTTATCAT AACATTT CT GTAA	
GCPS18-129Sam-ba2	TCGTAACGAC CTACAGAATA GAGTTATCAT AACATTTCT G AA	
GCPR18-3129R211-ba2	TGGTAACGGC CTCAAAAA.A GAGGTATCAA AAC.TTTTCT GT.A	
GCP18-10129R20-ba2	TGATAACGC C.CAAAAA.A AAGGT..CAA AACTT.TCCG GTAA	
Consensus	.....	.....
	151	200
EMBH44836anti	.....	.....
GCP18-5CP418L-Sams	.TATTTCCAT CAAAATGA.. CTAGAGAAC AGCAGTTCTT ATAACATTAT	
GCP18-2CP418L-Wes	.TATTTCCAT CAAAATGA.. CTAGAGAAC AG.AGTTCTT ATAACATTAT	
GCP18-4CP418L-R2000	ATATTTCCAT CAAAATGA.. CTAGAGAAC AG.AGTTCTT ATAACATTAT	
conse129bal-Drak	ATATTTCCAT CAAAATGA.. CTAGAGAAC AG.AGTTCTT ATAACATTAT	
GCPS18-129Sam-ba2	ATGTTTCCAT CAAAATGA CTATCGAAC ATAATTAAT ATA.CATTTT	
GCPR18-3129R211-ba2	ATGTTTCCAT CAAAATG. CTATCGGAC ATAATTAAT ATAAC.TTCT	
GCP18-10129R20-ba2	ATGTTTCCAT CAAAATG. CTTCGGA.C ATAATTAAT ATAAC.TTCT	
Consensus	ATGTTTCCCT CAAA.TGG CTTCGGA.C ATAATTAA A...CATTT	
	201	250
EMBH44836anti	.....	.....
GCP18-5CP418L-Sams	CTGTAAA TG.TTCCAA CAAAA CCACT ACATAGCAGAGTTC .TTATAACAT	
GCP18-2CP418L-Wes	CTGTAAA TG.TTCCAA CAAAA CCACT ACATAGCAGAGTTC ATTATAACAT	
GCP18-4CP418L-R2000	CTGTAAA TG.TTCCAA CAAAA CCACT ACATAGCAGAGTTC .TTATAACAT	
conse129bal-Drak	CTGTAAA TG.TTCCAA CAAAA CCACT ACATAGCAGAGTTC .TTATAACAT	
GCPS18-129Sam-ba2	CTG. AAAATATTCCCT CAAAA TTA. .CATTT TTT TTA.CAA.A.	
GCPR18-3129R211-ba2	CTG. AAAATATTCCCT CAAAA TTA. ACATTT TTT T.ACAA.A.	
GCP18-10129R20-ba2	CTG. AAA.TAATTCCT CAAAA TTA. ACATTT TTT T.ACAA.A.	
Consensus	.....	.....
	251	300
EMBH44836anti	.....	.....
GCP18-5CP418L-Sams	TGTCTGT.AA ATGTCCAATC AAAACCACTA CAGAACAAG CTCCTATAAC	
GCP18-2CP418L-Wes	TGTCTGT.AA ATGTCCAATC AAAACCACTA CAGAACAAG CTCCTATAAC	
GCP18-4CP418L-R2000	TGTCTGT.AA ATGTCCAATC AAAACCACTA CAGAACAAG CTCCTATAAC	
conse129bal-Drak	TGTCTGT.AA ATGTCCAATC AAAACCACTA CAGAACAAG CTCCTATAAC	
GCPS18-129Sam-ba2	TGTTTC... CATCAAAATG AGACTCA.G	
GCPR18-3129R211-ba2	TGTTTC... CATCAAAATG AGACTCA.G	
GCP18-10129R20-ba2	TGTTTC... CATCAAAATG AGACTCA.G	
Consensus	tttctgt.aa tgtttccatc aaaatgacta tcgaacataa ttaataaac	
	301	350
EMBH44836anti	A TTGTTT ATACAAAGTT TCACT AAAT CTACAAACTT CCCCCGTAAA	
GCP18-5CP418L-Sams	A TTGTTT ATACAAAGTTT .CACT AAAT CTACAAACTT TCCCCGTAAA	
GCP18-2CP418L-Wes	A TTGTTT ATACAAAGTT TCACT AAAT CTACAAACTT TCCCCGTAAA	
GCP18-4CP418L-R2000	A TTGTTT ATACAAAGTTT .CACT AAAT CTACAAACTT TCCCCGTAAA	
conse129bal-Drak	A TTGTTT ATACAAAGTT TCACT AAAT CTACAAACTT TCCCCGTAAA	
GCPS18-129Sam-ba2	AAC.CAGTTC TTGCAATAGTT TCACTTAAAT CTACAAACTT TC.....	
GCPR18-3129R211-ba2	AACACAGTTC TTGCAATAGTT TCACT.AAAT CTACAAACTT TC.....	
GCP18-10129R20-ba2	A.CCCAGTTC TTGCAATAGTT TC.CT.AAAT CTTCAAACTT TC.....	
Consensus	.....	.....

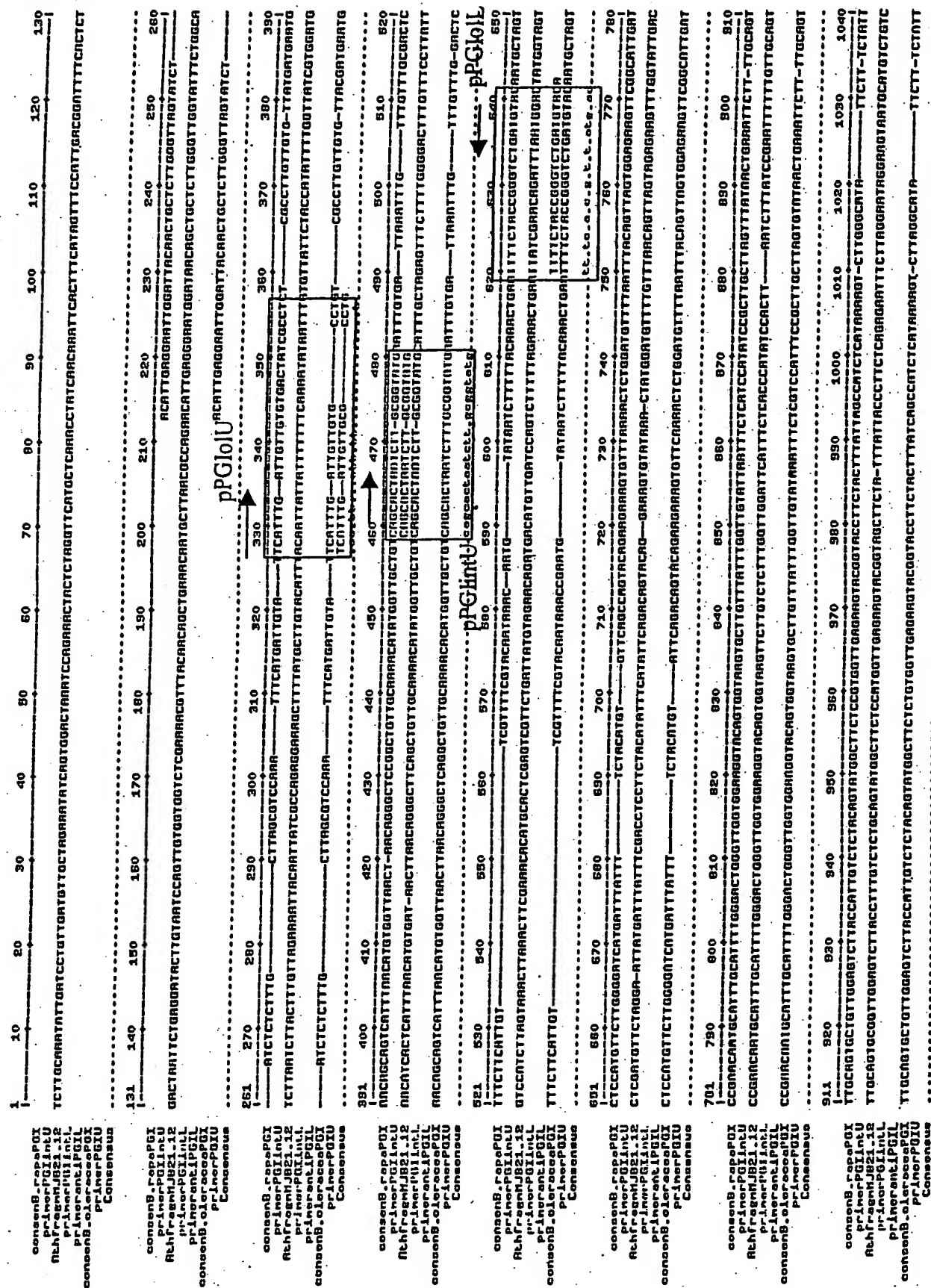
Figure 15 (b)

	351		400
EMBH44836anti	351		
GCP18-5CP418L-Sams	351		
GCP18-2CP418L-Wes	351		
GCP18-4CP418L-R2000	351		
conse129ba1-Drak	351		
GCP18-129Sam-ba2	351		
GCP18-3129R211-ba2	351		
GCP18-10129R20-ba2	351		
Consensus	351		
	401		
EMBH44836anti	401		
GCP18-5CP418L-Sams	401		
GCP18-2CP418L-Wes	401		
GCP18-4CP418L-R2000	401		
conse129ba1-Drak	401		
GCP18-129Sam-ba2	401		
GCP18-3129R211-ba2	401		
GCP18-10129R20-ba2	401		
Consensus	401		
	431		480
EMBH44836anti	431		
GCP18-5CP418L-Sams	431		
GCP18-2CP418L-Wes	431		
GCP18-4CP418L-R2000	431		
conse129ba1-Drak	431		
GCP18-129Sam-ba2	431		
GCP18-3129R211-ba2	431		
GCP18-10129R20-ba2	431		
Consensus	431		
	481		530
EMBH44836anti	481		
GCP18-5CP418L-Sams	481		
GCP18-2CP418L-Wes	481		
GCP18-4CP418L-R2000	481		
conse129ba1-Drak	481		
GCP18-129Sam-ba2	481		
GCP18-3129R211-ba2	481		
GCP18-10129R20-ba2	481		
Consensus	481		
	531		580
EMBH44836anti	531		
GCP18-5CP418L-Sams	531		
GCP18-2CP418L-Wes	531		
GCP18-4CP418L-R2000	531		
conse129ba1-Drak	531		
GCP18-129Sam-ba2	531		
GCP18-3129R211-ba2	531		
GCP18-10129R20-ba2	531		
Consensus	531		
	581		630
EMBH44836anti	581		
GCP18-5CP418L-Sams	581		
GCP18-2CP418L-Wes	581		
GCP18-4CP418L-R2000	581		
conse129ba1-Drak	581		
GCP18-129Sam-ba2	581		
GCP18-3129R211-ba2	581		
GCP18-10129R20-ba2	581		
Consensus	581		

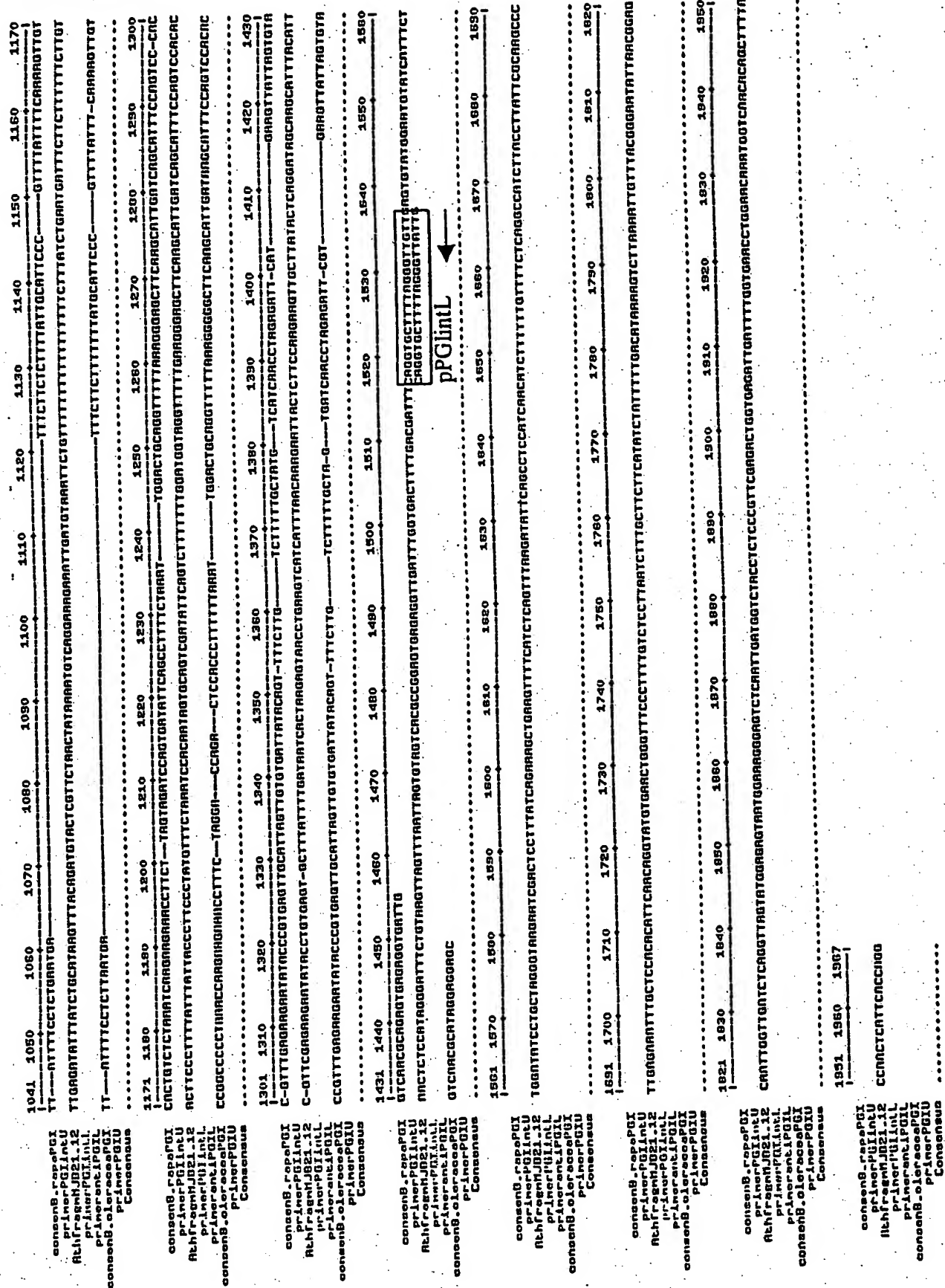
Figure 15 (c)

	631				690
EMBH44836anti	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT	TCGACGAAGA	GTGGAAGAGG
GCP18-5CP418L-Sams	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT	TCGACGAAGA	GTGGAAGAGG
GCP18-2CP418L-Wes	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT	TCGACGAAGA	GTGGAAGAGG
GCP18-4CP418L-R2000	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT	TCGACGAAGA	GTGGAAGAGG
consel29ba1-Drak	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT	TCGACGAA.A	GTGGAAGAGG
GCP18-129Sam-ba2	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT	TCGACGAAGA	GAGGAAGAGG
GCP18-3129R211-ba2	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT	TCGACGAAGA	GAGGAAGAGG
GCP18-10129R20-ba2	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT	TCG.CGAAGA	GAGGAAGAGG
Consensus	ggagcg.tgg	.aaaagagag	tggcacgatt	tcgacgaaga	g.ggaagagg
	691				740
EMBH44836anti	AGAGGGTGGT	GGATAAACTC	GCGTATGATC	AAGTTCGTCA	TCGTCCTGAT
GCP18-5CP418L-Sams	AGAGGGTGGT	GGATAAACTC	GCGTATGATC	AAGTTCGTCA	TCGTCCTGAT
GCP18-2CP418L-Wes	AGAGGGTGGT	GGATAAACTC	GCGTATGATC	AAGTTCGTCA	TCGTCCTGAT
GCP18-4CP418L-R2000	AGAGGGTGGT	GGATAAACTC	GCGTATGATC	AAGTTCGTCA	TCGTCCTGAT
consel29ba1-Drak	AGAGGGTGGT	GGATAAACTC	GCGTATGATC	AAGTTCGTCA	TCGTCCTGAT
GCP18-129Sam-ba2	AGAGGGTGGT	GGATAAACTC	GCGTATGATC	AAGTTCGTCA	TCGTCCTGAT
GCP18-3129R211-ba2	AGAGG.TGGT	GGATAAACTC	GCGTATGATC	AAGTTCGTCA	TCGTCCTGAA
GCP18-10129R20-ba2	AGAGGGTGGT	GGATAAACTC	GCGTATGATC	AAGTTCGTCA	TCGTCCTGAA
Consensus	agaggggtggt	ggataaaactc	gcgtatgatc	aagttcgtca	tcgtcctga.
	741			pSG129antiU	790
EMBH44836anti	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG	TGGCTTAGAA	GTTTCCGATG
GCP18-5CP418L-Sams	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG	TGGCTTAGAA	GTTTCCGATG
GCP18-2CP418L-Wes	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG	TGGCTTAGAA	GTTTCCGATG
GCP18-4CP418L-R2000	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG	TGGCTTAGAA	GTTTCCGATG
consel29ba1-Drak	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG	.GGCTTAGAA	GTTTCCGA..
GCP18-129Sam-ba2	TGCCGCCATT	CTTGTTTAC.	.GGCGCTCTG	GGT.....	.....
GCP18-3129R211-ba2	TGCCGCC...	.....	.....	.....	.....
GCP18-10129R20-ba2	TGCC..CAT.	CTTGAGCTC.	.GG.GCGCGG	GCTCACAA..	.....
Consensus	tgccgccat.	.tt.....c.	.gg.gc.c.g	.....	.....
	791				800
EMBH44836anti	TCAATGAAC	A	GTGACACGAC	GAAATGC	
GCP18-5CP418L-Sams	TCAATGAAC	AGAAT...	TC	CGGG...	
GCP18-2CP418L-Wes	CCAATGAACA	AGATTATTTT	CGATG..		
GCP18-4CP418L-R2000	.....	.....	.....		
consel29ba1-Drak	.....	.....	.....		

## Figure 16



## Figure 16<sup>BIS</sup>

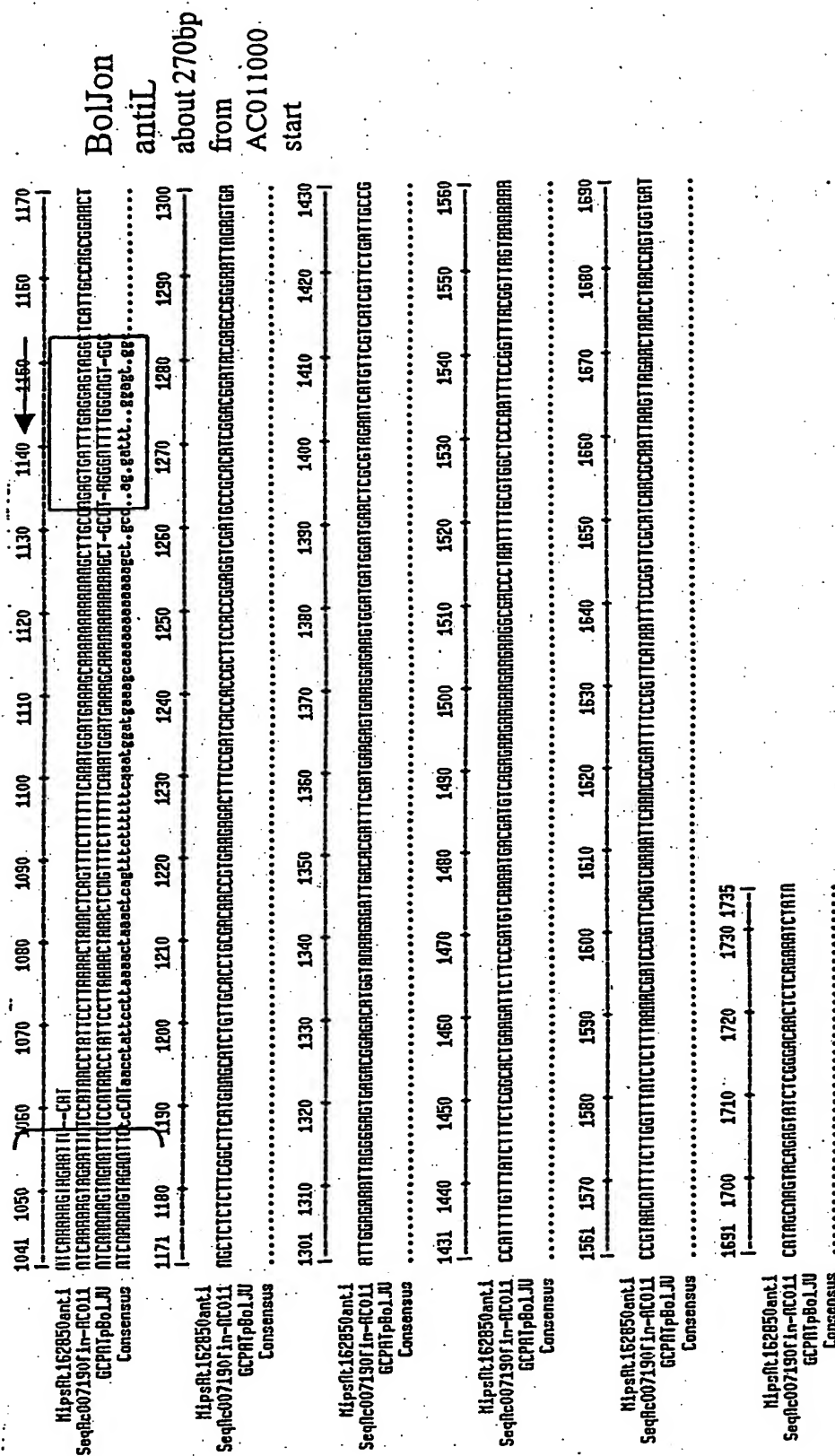




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**Figure 17** <sup>BIS</sup>



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